In the Sequence Listing:

Please insert the attached paper copy of the Sequence Listing as new pages 1-16 in the above-captioned application. A computer-readable copy (CFR copy) of the Sequence Listing accompanies this response.

Amendments

In the Specification:

Please replace the paragraph beginning at page 3, line 2, with the following rewritten paragraph:

--Figures 1A-1M show the nucleotide sequence (SEQ ID NO:1) and deduced amino acid sequence (SEQ ID NO:2) of cDNA encoding the BT-R_1 protein from *M. sexta*.--

Please replace the paragraph beginning at page 3, line 4, with the following rewritten paragraph:

--Figures 2A-2H show the deduced amino acid sequence of cDNA encoding the BT-R_1 protein from *M. sexta* (SEQ ID NO:2). Figure 2I shows a comparison of amino acid sequences of cadherin motifs (BTRcad-1 to 11) in BT-R_1 to those of other cadherins (SEQ ID NOS:8-11).--

Please replace the paragraph beginning at page 5, line 20, with the following rewritten paragraph:

--One class of BT-R_1 allelic variants will be proteins that share a high degree of homology with at least a small region of the amino acid sequence provided in Seq. ID No:2, but may further contain a radical departure from the sequence, such as a non-conservative substitution, truncation, insertion or frame shift. Such alleles are termed mutant alleles of BT-R_1

and represent proteins that typically do not perform the same biological functions as does the BT-R_1 variant of Seq. ID No:2. --

Please replace the paragraph beginning at page 29, line 3, with the following rewritten paragraph:

--The purified electroeluted BT-R_1 was subjected to cyanogen bromide digestion and the cyanogen bromide fragments separated on a 17% high-resolution tricine SDS-polyacrylamide gel as described by Schagger, H. *et al. Anal Biochem* (1987) 166:368. The separated fragments were transferred to Problott membranes (Applied Biosystems) and five bands were extracted and subjected to microsequencing using standard instrumentation. The amino acid sequences obtained were:

1. (Met)-Leu-Asp-Tyr-Glu-Val-Pro-Glu-Phe-Gln-Ser-Ile-Thr-Ile-Arg-Val-Val-Ala-Thr-Asp-Asn-Asn-Asp-Thr-Arg-His-Val-Gly-Val-Ala (SEQ ID NO:3);
2. (Met)-X-Glu-Thr-Tyr-Glu-Leu-Ile-Ile-His-Pro-Phe-Asn-Tyr-Tyr-Ala (SEQ ID NO:4);
3. (Met)-X-X-X-His-Gln-Leu-Pro-Leu-Ala-Gln-Asp-Ile-Lys-Asn-His (SEQ ID NO:5);
4. (Met)-Phe/Pro-Asn/Ile-Val-Arg/Tyr-Val-Asp-Ile/Gly (SEQ ID NO:6);
5. (Met)-Asn-Phe-Phe/His-Ser-Val-Asn-Arg/Asp-Glu (SEQ ID NO:7). --

Please replace the paragraph beginning at page 30, line 14, with the following rewritten paragraph:

--As shown in Figures 2A-2H, the deduced amino acid sequence includes a putative signal, shown underlined, preceding the mature N-terminus Asn-Glu-Arg-etc. Eleven repeats (cad1-cad11) are shown in the extracellular region upstream of the membrane domain, shown with the heavy underline, at positions 1406-1427 (SEQ ID NO:2). The end of the 11th repeat is

shown with an arrowhead. The positions of the five CNBR fragments are also shown under the complete sequence.

Please replace the paragraph beginning at page 30, line 20, with the following rewritten paragraph:

--Figure 2I compares the BT-R_1 sequence obtained herein (SEQ ID NO:2) with other members of the cadherin family. Like known cadherins, the external domain of BT-R_1 is highly repetitive and contains 11 repeats (cad1-cad11; see Figure 2 I). The other cadherins compared in Figure 2 I are mouse P cadherin (mP EC1); *Drosophila fat* EC18 (fat EC18) and protocadherin (PC42 EC2), and *Manduca sexta* intestinal transporter (HPT-1-EC-1). The eleven repeats of the cadherin motif in BT-R_1 (cad1-cad11) are individually aligned with a single motif sequence from each of the other members of the cadherin family. Conserved residues are boxed. The greatest similarity of BT-R_1 to the cadherins is with the extracellular repeats of the cadherin motif of mouse P-cadherin, Drosophila *fat* tumor suppressor and the protocadherins, although homologies are not high (20-40 homology and 30-60 percent similarity). The conserved repeats of BT-R_1 included AXDXD (SEQ ID NO.12), DXE, DXNDXXP (SEQ ID NO:13), one glutamic acid residue and two glycine residues (Figure 2 I). Motifs A/VXDXD (SEQ ID NO:14), DXNDN (SEQ ID NO:15) are the consensus sequences for calcium binding and two such regions are present in a typical cadherin repeat. In all repeats of BT-R_1, the sequence DXNDN (SEQ ID NO:15) is preceded by 8 to 14 hydrophobic amino acids. Similar hydrophobic sequences also have been observed in the cadherins. The length of the hydrophobic stretches suggests that these areas are not transmembrane regions buy that the represent J-sheet structures commonly present in cadherin-like repeats. BT-R_1 contains a putative cytoplasmic domain of 101 amino acids, smaller than vertebrate cadherin cytoplasmic domains (160 amino acids), and shows no homology to any of the cadherin cytoplasmic domains or to cytoplasmic domains of other proteins to which it has been compared in a current sequence data base.--